In the Specification:

Please delete the current paper sequence listing and insert in its place the attached new paper sequence listing.

At page 1 of the specification, please delete the current tile of the invention and replace it with the following new title:

METHOD FOR TREATING A MAMMAL BY ADMINISTERING A COMPOUND THAT MODULATES THE BIOLOGICAL ACTIVITY OF ABC1

Please amend the paragraph on page 1, starting at line 23, as follows:

Epidemiological studies have consistently demonstrated that plasma HDL-C [)] concentration is inversely related to the incidence of CAD. HDL-C levels are a strong graded and independent cardiovascular risk factor. Protective effects of an elevated HDL-C persist until 80 years of age. A low HDL-C is associated with an increased CAD risk even with normal (<5.2 mmol/l) total plasma cholesterol levels. Coronary disease risk is increased by 2% in men and 3% in women for every 1 mg/dL (0.026 mmol/l) reduction in HDL-C and in the majority of studies this relationship is statistically significant even after adjustment for other lipid and non-lipid risk factors. Decreased HDL-C levels are the most common lipoprotein abnormality seen in patients with premature CAD. Four percent of patients with premature CAD with have an isolated form of decreased HDL-C levels with no other lipoprotein abnormalities while 25% have low HDL levels with accompanying hypertriglyceridemia.

Please amend the paragraph on page 17, lines 6-10, as follows:

Fig. 1C shows ApoAI (10 μg/mL) -mediated cellular cholesterol efflux in control fibroblasts (n=5, normalized to 100%) and two subjects with Tangier disease (TD).

Cells were ^{3}H-cholesterol (0.2 µCi/mL ~~□Ci/mL~~) labeled during growth and cholesterol (20 µg/mL ~~□g/mL~~) loaded in growth arrest. Cholesterol efflux is determined as ^{3}H medium/(^{3}H cell + ^{3}H medium)

Please amend the paragraph on page 18, lines 8-11, as follows:

Fig. 4A shows sequence (SEQ ID NO: 39) of one mutation in family TD-1. Patient III-01 is heterozygous for a T to C transition at nucleotide 4503 of the cDNA; the control (SEQ ID NO: 38) is homozygous for T at this position. This mutation corresponds to a cysteine to arginine substitution in the ABC1 protein (C1477R).

Please amend the paragraph on page 18, lines 13-20, as follows:

Fig 4B shows the amino acid sequence conservation of residue 1477 in mouse and human, but not a related *C. elegans* gene. A change from cysteine to arginine likely has an important effect on the protein secondary and tertiary structure, as noted by its negative scores in most substitution matrices (Schuler et al., A Practical Guide to the Analysis of Genes and Proteins, eds. Baxevanis, A.D. & Ouellette, B.F.F. 145:171, 1998). The DNA sequences of the normal and mutant genes are shown above and below the amino acid sequences, respectively. The sequences shown are from top to bottom: wt sequence (SEQ ID NO: 40), human ABC1 (SEQ ID NO: 41), mouse ABC1 (SEQ ID NO: 42), Patient (SEQ ID NO: 43), CAEEL-ABC (SEQ ID NO: 44) and Patient (SEQ ID NO: 45).

Please amend the paragraph on page 19, lines 7-10, as follows:

Fig. 5A shows the sequence (SEQ ID NO: 47) of the mutation in family TD-2.

Patient IV-10 is homozygous for an A to G transition at nucleotide 1864 of the cDNA (SEQ ID NO: 2); the control (SEQ ID NO: 46) is homozygous for A at this position. This mutation corresponds to a glutamine to arginine substitution in the ABC1 protein (Q597R).

Please amend the paragraph on page 19, lines 12-17, as follows:

Fig. 5B shows that the glutamine amino acid, which is mutated in the TD-2 proband, is conserved in human and mouse ABC1 as well as in an ABC orthologue from *C. elegans,* revealing the specific importance of this residue in the structure/function of this ABC protein in both worms and mammals. The DNA sequences of the normal and mutant proteins are shown above and below the amino acid sequences, respectively. The sequences shown are from top to bottom: wt sequence (SEQ ID NO: 48), human ABC1 (SEQ ID NO: 288), mouse ABC1 (SEQ ID NO: 289), Patient (SEQ ID NO: 290), CAEEL-ABC (SEQ ID NO: 52) and Patient (SEQ ID NO: 53).

Please amend the paragraph on page 20, lines 1-5, as follows:

Fig. 6A shows a sequence (SEQ ID NO: 55) of the mutation in family FHA-1. Patient III-01 is heterozygous for a deletion of nucleotides 2151-2153 of the cDNA (SEQ ID NO: 2). This deletion was detected as a superimposed sequence starting at the first nucleotide after the deletion. This corresponds to deletion of leucine 693 in the ABC1 protein (SEQ ID NO: 1).

Please amend the paragraph on page 20, lines 7-12, as follows:

Fig. 6B is an alignment of the human and mouse wild-type amino acid sequences, showing that the human and mouse sequences are identical in the vicinity of L693. L693 is also conserved in *C. elegans*. This highly conserved residue lies within a predicted transmembrane domain. The DNA sequences of the normal and mutant proteins are shown above and below the amino acid sequences, respectively. The sequences shown are from top to bottom: wt sequence (SEQ ID NO: 55), human ABC1 (SEQ ID NO: 56), mouse ABC1 (SEQ ID NO: 57), Patient (SEQ ID NO: 58), CAEEL-ABC (SEQ ID NO: 59) and Patient (SEQ ID NO: 60).

Please amend the paragraph on page 20, lines 23-27, as follows:

Fig. 6D shows a sequence (SEQ ID NO: 61) of the mutation in family FHA-3. Patient III-01 is heterozygous for a deletion of nucleotides 5752-5757 of the cDNA (SEQ ID NO: 2). This deletion was detected as a superimposed sequence starting at the first nucleotide after the deletion. This corresponds to deletion of glutamic acid 1893 and aspartic acid 1894 in the ABC1 protein (SEQ ID NO: 1).

Please amend the paragraph on page 20, lines 7-12, as follows:

Fig. 6E is an alignment of the human and mouse wild-type amino acid sequences, showing that the human and mouse sequences are identical in the vicinity of 5752-5757. This region is highly conserved in *C. elegans*. The DNA sequences of the normal and mutant proteins are shown above and below the amino acid sequences, respectively. The sequences shown are from top to bottom: wt sequence (SEQ ID NO: 62), human ABC1 (SEQ ID NO: 63), mouse ABC1 (SEQ ID NO: 64), Patient (SEQ ID NO: 65), CAEEL-ABC (SEQ ID NO: 66) and deletion (SEQ ID NO: 67).

Please amend the paragraph on page 21, lines 4-8, as follows:

Fig. 6F shows a sequence (SEQ ID NO: 69) of the mutation in family FHA-2. Patient III-01 is heterozygous for a for a C to T transition at nucleotide 6504 of the cDNA (SEQ ID NO: 2). This alteration converts an arginine at position 2144 of SEQ ID NO: 1 to a STOP codon, causing truncation of the last 118 amino acids of the ABC1 protein. The control sequence at the top is SEQ ID NO: 68.

Please amend the paragraph on page 21, lines 10-25, as follows:

Figs. 7A and 7B show cholesterol efflux from human skin fibroblasts treated with ABC1 antisense oligonucleotides. Fibroblasts from a control subject were labeled with ^{3}H cholesterol (0.2 ~~□Ci/mL~~ μCi/mL) during growth for 48 hours and transfected with 500 nM *ABC1* antisense AN-1 (5'-GCA GAG GGC ATG GCT TTA TTT G-3'; SEQ ID NO: 3) with 7.5 μg lipofectin for 4 hours. Following transfection, cells were cholesterol loaded (20 μg/mL) for 12 hours and allowed to equilibrate for 6 hours. Cells were either then harvested for total RNA and 10 ~~□g~~ μg was used for Northern blot analysis. Cholesterol efflux experiments were carried out as described herein. Fig. 7A: AN-1 was the oligonucleotide that resulted in a predictable decrease in *ABC1* RNA transcript levels. Fig. 7B: A double antisense transfection method was used. In this method, cells were labeled and transfected with AN-1 as above, allowed to recover for 20 hours, cholesterol loaded for 24 hours, and then re-transfected with AN-1. Twenty hours after the second transfection, the cholesterol efflux as measured. A ~50% decrease in *ABC1* transcript levels was associated with a significant decrease in cholesterol efflux intermediate between that seen in wild-type and TD fibroblasts.

Please amend the paragraph on page 23, lines 10-12, as follows:

Fig. 14 is a schematic illustration showing that the WHAM chicken contains a non-conservative substitution (G265A) resulting in an amino acid change (E89K). The control sequence is shown at the top (SEQ ID NO: 276) while the WHAM mutation is shown at the bottom (SEQ ID NO: 277).

Please amend the paragraph on page 23, lines 14-16, as follows:

Fig. 15 is a schematic illustration showing that the mutation in the WHAM chicken is at an amino acid that is conserved among human, mouse, and chicken. The sequences shown are from top to bottom: wt chicken nucleotide (SEQ ID NO: 278), human ABC1 (SEQ ID NO: 279), mouse ABC1 (SEQ ID NO: 280), wt chicken amino acid (SEQ ID NO: 281), WHAM chicken nucleotide (SEQ ID NO: 282) and WHAM chicken nucleotide (SEQ ID NO: 283).